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============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2010; month=9; day=22; hr=13; min=17; sec=57; ms=554; ]
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                      Validated By CRFValidator v 1.0.3

Application No:           09910208              Version No:           6.0


                   Input Set:


                   Output Set:



             Started:   2010-09-14 13:00:40.902
            Finished:   2010-09-14 13:00:42.615
             Elapsed:   0 hr(s) 0 min(s) 1 sec(s) 713 ms
      Total Warnings:   14
        Total Errors:   2
  No. of SeqIDs Defined:   20
    Actual SeqID Count:    20
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Error code        Error Description

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W  213        Artificial or Unknown found in <213>  in SEQ ID (8)

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W  213        Artificial or Unknown found in <213>  in SEQ ID (10)

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W  213        Artificial or Unknown found in <213>  in SEQ ID (18)

W  402        Undefined organism found in <213>  in SEQ ID (19)

E  257        Invalid sequence data feature in <221>  in SEQ ID (19)

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SEQUENCE LISTING

<110>  Hitomi, Ji ro

       Yamamura, Tokujiro

       Kimura, Tatsuji

       Yamaguchi, Ken

<120>  Novel calcium-Binding Proteins

<130>  MM4454

<140>  09910208
<141>  2001-07-20


<160>  20

<170>  PatentIn version 3.5

<210>  1
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<213>  Bovine calcium binding protein


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<222>  (48)..(323)

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                                                     Met Thr Lys
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ctg gaa gat cac ctg gag gga atc atc aac atc ttc cac cag tac tcc         104
Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln Tyr Ser
    5                  10                  15


gtt cgg gtg ggg cat ttc gac acc ctc aac aag cgt gag ctg aag cag        152
Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu Lys Gln
20                  25                  30                  35


ctg atc aca aag gaa ctt ccc aaa acc ctc cag aac acc aaa gat caa        200
Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp Gln
                40                  45                  50


cct acc att gac aaa ata ttc caa gac ctg gat gcc gat aaa gac gga        248
Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys Asp Gly
                55                  60                  65


gcc gtc agc ttt gag gaa ttc gta gtc ctg gtg tcc agg gtg ctg aaa        296
Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val Leu Lys
            70                  75                  80


aca gcc cac ata gat atc cac aaa gag taggaagctc tttccagcaa              343
Thr Ala His Ile Asp Ile His Lys Glu
            85                  90

tgtccccaag aagacttacc cttctcctcc ctgaggctgc cttacccgag ggaagagaga 403

attaataaac gtactttggc aaagtt 429


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<212> PRT
<213> Bos taurus

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Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
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Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
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Asp Gln Pro
    50


<210> 3
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<213> Bos taurus

<400> 3

Ile Phe Gln Asp Leu Asp Ala Asp
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<210> 4
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<400> 4

Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu
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<400> 5

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1               5


<210>   6
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<212>   PRT
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<400>   6

Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp Gln Pro Thr Ile Asp Lys
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Ile Phe Gln Asp Leu Asp Ala Asp Lys Asp Gly Ala Val Ser Phe
            20                  25                  30


<210>   7
<211>   20
<212>   PRT
<213>   Bos taurus

<400>   7

Glu Phe Val Val Leu Val Ser Arg Val Leu Lys Thr Ala His Ile Asp
1               5                   10                  15


Ile His Lys Glu
            20


<210>   8
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<220>
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<400> 11
ttgacaccag accaactggt aatg                                              24


<210> 12
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<213> Human calcium-binding protein


<220>
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<222> (22)..(297)
<223> Deduced amino acid sequence for human calcium-binding protein

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                        Met Thr Lys Leu Glu Glu His Leu Glu Gly

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                 1                   5                          10
att gtc aat atc ttc cac caa tac tca gtt cgg aag ggg cat ttt gac       99
Ile Val Asn Ile Phe His Gln Tyr Ser Val Arg Lys Gly His Phe Asp
                   15                  20                  25

acc ctc tct aag ggt gag ctg aag cag ctg ctt aca aag gag ctt gca      147
Thr Leu Ser Lys Gly Glu Leu Lys Gln Leu Leu Thr Lys Glu Leu Ala
             30                  35                  40

aac acc atc aag aat atc aaa gat aaa gct gtc att gat gaa ata ttc      195
Asn Thr Ile Lys Asn Ile Lys Asp Lys Ala Val Ile Asp Glu Ile Phe
         45                  50                  55

caa ggc ctg gat gct aat caa gat gaa cag gtc gac ttt caa gaa ttc      243
Gln Gly Leu Asp Ala Asn Gln Asp Glu Gln Val Asp Phe Gln Glu Phe
     60                  65                  70

ata tcc ctg gta gcc att gcg ctg aag gct gcc cat tac cac acc cac      291
Ile Ser Leu Val Ala Ile Ala Leu Lys Ala Ala His Tyr His Thr His
75                  80                  85                  90

aaa gag taggtagctc tctgaagctt tttacccagc aatgtcctca atgagggtct       347
Lys Glu

tttctttccc tcaccaaaac ccagccttgc ccgtggggag taagagttaa taaacacact     407

cacgaaaagt taaaaaaaaa aaaaaaaaat tct                                  440


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<220>
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<400>  13
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<210>  14
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<210>  15
<211>  15
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<212> DNA
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<220>
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<210> 16
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<210> 17
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<220>
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<400> 18
ggacattgct gggtaaaaag                                                     20


<210> 19
<211> 92
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<222> (1)..(92)

<400> 19

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1               5                   10                  15


Gln Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu
            20                  25                  30


Leu Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr
        35                  40                  45


Lys Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp
    50                  55                  60


Lys Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg
65                  70                  75                  80


Val Leu Lys Thr Ala His Ile Asp Ile His Lys Glu
                85                  90



<210>   20
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<212>   PRT
<213>   human calcium binding protein


<220>
<221>   Amino acid sequence of SEQ 1D NO. 12
<222>   (1)..(92)


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Gln Tyr Ser Val Arg Lys Gly His Phe Asp Thr Leu Ser Lys Gly Glu
            20                  25                  30


Leu Lys Gln Leu Leu Thr Lys Glu Leu Ala Asn Thr Ile Lys Asn Ile
        35                  40                  45


Lys Asp Lys Ala Val Ile Asp Glu Ile Phe Gln Gly Leu Asp Ala Asn
    50                  55                  60


Gln Asp Glu Gln Val Asp Phe Gln Glu Phe Ile Ser Leu Val Ala Ile
65                  70                  75                  80
```

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Ala Leu Lys Ala Ala His Tyr His Thr His Lys Glu
            85                    90
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